wherein an alteration in the expression of said one or more genes in each cell type in the presence of the test compound relative to the expression of said one or more genes in each cell type in the absence of the test compound indicates the function of said test compound.

A1 cont.

2. (Amended) The method of claim 1, wherein expression of at least two genes is measured in each cell type.

3. (Amended) The method of claim 1, wherein expression of at least five genes is measured in each cell type.

6. (Amended) The method of claim 1, wherein said method further comprises measuring the expression of one or more genes in a fourth cell type.

A2

7. (Amended) The method of claim 1 or 6, wherein said method further comprises measuring the expression of three or more genes in each cell type.

A3

10. (Amended) The method of claim 1, wherein said cell types are provided in a container.

11. The method of claim 1, wherein expression of one or more of said genes is compared to expression of a reference gene.

12. The method of claim 11, wherein said test compound modulates expression of said one or more genes at least four-fold relative to said reference gene.

13. The method of claim 1, wherein said test compound is a polypeptide.

14. (Amended) The method of claim 1, wherein said method comprises contacting the cell types with two or more test compounds.

A4

15. (Amended) The method of claim 1, wherein said cell types comprise human cells.

A5

17. (Amended) The method of claim 1, wherein said three cell types are selected from the group consisting of MG-63 cells, U87-MG cells, TF-1 cells, HepG2 cells, THP-1 cells, HUVEC cells, CCD-1070SK cells, and Jurkat E6-1 cells.

18. The method of claim 1, wherein expression of one or more sequences is measured using real-time polymerase chain reaction.

19. (Amended) A method of identifying the function of a polypeptide test compound, the method comprising:

providing at least three mammalian cell types, wherein the cell types comprise osteosarcoma, astrocytoma, erythroleukemia, hepatoma, monocytic, endothelial, fibroblast, T-cell, monocyte, B-cell, NK-cell, normal human osteoblast, astrocyte, hepatocyte and normal human lung fibroblast cell types;

A6

contacting each of the cell types with said polypeptide; and

measuring expression of three more genes in each cell type,

wherein an alteration in the expression of said genes in each cell type in the presence of the polypeptide relative to the expression of said genes in each cell type in the absence of the test compound indicates the function of said test compound.

20. The method of claim 19, wherein expression of said genes is measured using real-time polymerase chain reaction.

REMARKS

In the Office Action dated September 12, 2002 ("Office Action"), the Examiner made the following rejections:

(1) Claims 1-17 and 19 were rejected under 35 U.S.C. § 102(a) as being anticipated by Johnson et al. (WO 99/37817) ("Johnson");

(2) Claims 18 and 20 were rejected under 35 U.S.C. § 103(a) as being unpatentable over Johnson (WO 99/37817) in view of MacLeod et al. (USPN 6,221,600) ("MacLeod").